

SEQUENCE LISTING

<110> Ledbetter, Jeffrey

Hayden-Ledbetter, Martha

<120> Binding Domain-Immunoglobulin Fusion Proteins

<130> 390069.401

<140> US

<141> 2002-01-17

<150> US 09/765,208

<151> 2001-01-17

<160> 38

<170> PatentIn version 3.0

<210> 1

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<220>

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<223> light chain variable region for anti-CD20 scFv

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<223> heavy chain variable region for anti-CD20 scFv

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gacttgcagg gccagctcaa gtgtaagtta catgcactgg	240
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc	300
caacctgggt tctggagtcc ctgtctgctt cagtggcagt gggctctgga	360
cctcttactc tctcacaatc agcagagtgg aggctgaaga tgctgccact	420
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ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc	600
tgagctggtg aggcctgggg cctcagtga	660
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aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg	780
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812

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<223> SYNTHETIC MOUSE HUMAN CHIMERIC FUSION GENE

<220>

<221> misc_feature

<222> (13)..(807)

<223> MURINE ANTI-HUMAN CD20 scFv

<220>

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<222> (808)..(1513)

<223> HUMAN IgG1 Fc TAIL, WILD TYPE HINGE, CH2 AND CH3

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ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180

taccagcaga agccaggatc ctcccccaaa ccttgattt atgccccatc caacctgggt 240

tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc 300

agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360

cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgt 420

ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480

aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540

aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600

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<220>

<221> misc_feature

<222> (13)..(807)<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> C_region

<222> (808)..(1513)

<223> HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES
 PROLINE TO SERINE MUTATION (880-883) IN CH2 DISRUPTS EFFECTOR FUNCTION

<400> 3

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ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg      180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctgggt      240
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agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca      360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgt      420
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aggcctgggg cctcagtgaag gatgtcctgc aaggcttctg gctacacatt taccagttac      540
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ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta      660
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gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc     1140
aaciaaagccc tcccagcccc catcgagaaa acaatctcca aagccaaagg gcagccccga     1200
gaaccacagg tgtacacctt gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc     1260
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat     1320
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<221> misc_feature

<222> (13)..(807)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> C_region

<222> (808)..(1513)

<223> HINGE CYSTEINES MUTATED TO SERINES (826-829; 844-847; 853-856)
WILD TYPE CH2 AND CH3 DOMAINS MEDIATE EFFECTOR FUNCTIONS

<400> 4

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ccaggggaga aggtcacaat gacttgacagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctgggt 240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccac 360
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aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
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<223> MOUSE ANTI HUMAN CD20 SCFV

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<221> N_region

<222> (797)..(864)

<223> HUMAN IGA HINGE REGION

<220>

<221> C_region

<222> (865)..(1518)

<223> HUMAN IGG1 CH2 AND CH3 WILD TYPE FC DOMAIN

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gtcacaaatga cttgcagggc cagctcaagt gtaagttaca tgcactggta ccagcagaag      180
ccaggatcct cccccaacc ctggatttat gcccaccca acctggcttc tggagtcct      240
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gctgaagatg ctgccactta ttactgccag cagtggagtt ttaaccacc caggttcggt      360
gctgggacca agctggagct gaaagatggc ggtggctcgg gcggtggtgg atctggagga      420
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gcaagagtgg tgtactatag taactcttac tggctactcg atgtctgggg cacagggacc      780
acggtcaccg tctctgatca gccagttccc tcaactccac ctaccccatc tccctcaact      840
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ttccccccaa aacccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg      960
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gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag      1140
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<223> HINGE CYSTEINES MUTATED TO SERINES (19-21; 37-39; 46-48)

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tccgggaccc ctgaggtcac atgcgtgggt gtggacgtga gccacgaaga ccctgaggtc      180
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag      240
gagcagtaca acagcacgta ccgtgtgggt agcgtcctca ccgtcctgca ccaggactgg      300

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ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 360
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<223> HUMAN IGA HINGE

<220>

<221> C_region

<222> (70)..(723)

<223> HUMAN WILD TYPE IGG1 CH2 AND CH3, FC

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<223> LIGHT CHAIN LEADER PEPTIDE

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<222> (73)..(405)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

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<222> (406)..(450)

<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

<220>

<221> V_region

<222> (454)..(825)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

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<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

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<222> (73)..(393)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

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<222> (394)..(441)

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<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

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acgttcggtg gaggcaccga actggagatc aaaggtggcg gtggctcggg cggtggtggg	420
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<222> (1)..(61)

<223> native light chain leader peptide

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<223> (gly4ser)3 linker peptide

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<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

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<223> BclI restriction site

<400> 10
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aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggtcact 120
atgaactgta agtccagtc aagtgttttc tacagttcaa atcagaggaa ttatttggcc 180
tggtatcagc agaaaccagg gcagtctccc aaattgctga tctactgggc atctactagg 240
gaatctgggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactottacc 300
atcagcagtg tacatactga agacctggca gtttattact gtcacaaatt cctctcttcg 360
tggacgttcg gtggaggcac caagctggaa atcaaaggcg gtgggtgggtc ggggtgggtg 420
ggttcgggtg gcggcggatc ttctcaggtc caactgcagc agcctggggc tgaactgggtg 480
aagcctggga cttcagtga gctgtcctgc aaggcctctg gctacacctt caccaactac 540
tggatggtct ggggtgaagca gacgcctgga gaaggccttg agtggattgg agaaattatt 600
cctagcaacg gtctgtactaa atacaatgag aagttcaaga gcaaggccac actgactgca 660
gacaaatcct cccgcacagc ctacatgcaa ctcagcagcc tggcatctga ggactctgcg 720
gtctattatt gtgcaagaga gatgtccatt attactacgg tactgactcc cggtttgctt 780
actggggcca agggactctg gtcactgtct ctgcagcctg atca 824

<210> 11

<211> 266

<212> PRT

<213> Mus musculus

<220>

<221> INIT_MET

<222> (1)..(1)

<220>

<221> SIGNAL

<222> (1)..(22)

<220>

<221> DOMAIN

<222> (23)..(128)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<220>

<221> SITE

<222> (129)..(144)

<223> ASP-(GLY3SER)-(GLY4SER)2-SER LINKER PEPTIDE

<220>

<221> DOMAIN

<222> (145)..(266)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<400> 11

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser

50	55	60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro		
65	70	75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile		
	85	90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp		
	100	105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys		
	115	120 125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser		
	130	135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala		
	145	150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr		
	165	170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile		
	180	185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe		
	195	200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr		
	210	215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys		
	225	230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp		
	245	250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp		
	260	265

<210> 12

<211> 271

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(271)

<223> MOUSE ANTI-HUMAN CD19 SCFV

<400> 12

Met	Glu	Thr	Asp	Thr	Leu	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro
1				5					10					15	
Gly	Ser	Thr	Gly	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala
			20					25					30		
Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	Gln	Ser
		35					40					45			
Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Ile	Pro
	50					55					60				
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asn	Leu	Val	Ser
65					70					75					80
Gly	Ile	Pro	Pro	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
				85					90					95	
Leu	Asn	Ile	His	Pro	Val	Glu	Lys	Val	Asp	Ala	Ala	Thr	Tyr	His	Cys
			100					105					110		
Gln	Gln	Ser	Thr	Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu
		115					120					125			
Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
	130					135						140			
Gly	Ser	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg
145					150					155					160
Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe
				165					170					175	
Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu
			180					185					190		
Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	Asn	Tyr	Asn
	195						200					205			
Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	Ser	Ser	Ser
	210					215					220				
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	Ser	Ala	Val
225					230					235					240
Tyr	Phe	Cys	Ala	Arg	Arg	Glu	Thr	Thr	Thr	Val	Gly	Arg	Tyr	Tyr	Tyr
				245					250					255	
Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	
			260					265					270		

<210> 13

<211> 259

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(259)

<223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

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Met Val Ser Thr Ala Gln Phe Leu Gly Leu Leu Leu Leu Trp Leu Thr
1          5          10          15

Gly Gly Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
          20          25          30

Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn
          35          40          45

Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
50          55          60

Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser
65          70          75          80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser
          85          90          95

Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser
          100          105          110

Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly
          115          120          125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ala
          130          135          140

Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser
145          150          155          160

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
          165          170          175

Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
          180          185          190

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Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
 195                200                205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met
 210                215                220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
 225                230                235                240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
 245                250                255

Val Ser Ser

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<210> 14
<211> 272
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(272)
<223> MOUSE ANTI-HUMAN CD22 SCFV

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<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
 1          5          10          15

Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
 20          25          30

Val Ser Ala Gly Glu Lys Val Thr Met Asn Cys Lys Ser Ser Gln Ser
 35          40          45

Val Phe Tyr Ser Ser Asn Gln Arg Asn Tyr Leu Ala Trp Tyr Gln Gln
 50          55          60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 65          70          75          80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 85          90          95

Phe Thr Leu Thr Ile Ser Ser Val His Thr Glu Asp Leu Ala Val Tyr
 100         105         110

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Tyr Cys His Gln Phe Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys
 115 120 125
 Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140
 Gly Gly Ser Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val
 145 150 155 160
 Lys Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr
 165 170 175
 Phe Thr Asn Tyr Trp Met Val Trp Val Lys Gln Thr Pro Gly Glu Gly
 180 185 190
 Leu Glu Trp Ile Gly Glu Ile Ile Pro Ser Asn Gly Arg Thr Lys Tyr
 195 200 205
 Asn Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
 210 215 220
 Arg Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala
 225 230 235 240
 Val Tyr Tyr Cys Ala Arg Glu Met Ser Ile Ile Thr Thr Val Leu Thr
 245 250 255
 Pro Gly Leu Leu Thr Gly Ala Lys Gly Leu Trp Ser Leu Ser Leu Gln
 260 265 270

<210> 15

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

<400> 15

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
      20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
      35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
      50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
      85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
      100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
      115      120      125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
      130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
      165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
      180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
      195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
      210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
      245      250      255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys

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260					265					270					
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
		275					280					285			
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
	290					295					300				
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
305					310					315					320
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
			325					330						335	
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
			340					345					350		
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
		355					360					365			
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
	370					375					380				
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
385					390					395					400
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
			405					410						415	
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
		420					425						430		
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
		435					440					445			
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
	450					455					460				
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
465					470					475					480
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
			485						490					495	
Pro	Gly	Lys													

<210> 16

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>

<221> DOMAIN

<222> (265)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser	1	5	10	15
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	20	25	30	
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	35	40	45	
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	50	55	60	
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	65	70	75	80
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	85	90	95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	100	105	110	
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	115	120	125	
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	130	135	140	
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	145	150	155	160

Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr		
				165					170					175			
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile		
			180					185					190				
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe		
		195					200					205					
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr		
	210					215					220						
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys		
225					230					235					240		
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp		
				245					250					255			
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Asp	Gln	Glu	Pro	Lys	Ser	Ser		
			260					265					270				
Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Ala	Pro	Glu	Leu	Leu	Gly		
		275					280					285					
Gly	Ser	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met		
	290					295					300						
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His		
305					310					315					320		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val		
				325					330					335			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr		
			340					345					350				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly		
		355					360					365					
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile		
	370					375					380						
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val		
385					390					395					400		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser		
				405					410					415			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu		
			420					425					430				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro		
		435					440					445					
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val		
	450					455					460						

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495

Pro Gly Lys

<210> 17

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
 CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60

Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	65	70	75	80
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	85	90	95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	100	105	110	
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	115	120	125	
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	130	135	140	
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala	145	150	155	160
Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	165	170	175	
Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile	180	185	190	
Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe	195	200	205	
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	210	215	220	
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	225	230	235	240
Ala	Arg	Val	Val	Tyr	Tyr	Ser	Asn	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	245	250	255	
Gly	Thr	Gly	Thr	Thr	Val	Thr	Val	Ser	Asp	Gln	Glu	Pro	Lys	Ser	Ser	260	265	270	
Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Ala	Pro	Glu	Leu	Leu	Gly	275	280	285	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	290	295	300	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	305	310	315	320
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	325	330	335	
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	340	345	350	
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	355	360	365	

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
485 490 495

Pro Gly Lys

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(288)

<223> WILD TYPE IGA HINGE

<220>

<221> DOMAIN

<222> (289)..(505)

<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1          5          10          15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
          20          25          30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
          35          40          45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
          50          55          60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65          70          75          80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
          85          90          95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
          100          105          110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
          115          120          125

Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
          130          135          140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
          145          150          155          160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
          165          170          175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
          180          185          190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
          195          200          205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
          210          215          220

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr
 260 265 270
 Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Ser Cys
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 330 335
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 340 345 350
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 355 360 365
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 370 375 380
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 385 390 395
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 405 410 415
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 420 425 430
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 435 440 445
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 465 470 475
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 485 490 495
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505

<210> 19

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(234)

<223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)
WILD TYPE CH2 AND CH3 DOMAINS
ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp	Gln	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser			
1				5					10					15				
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro			
			20					25					30					
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys			
		35					40					45						
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp			
	50					55					60							
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu			
65					70					75					80			
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu			
				85					90					95				
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn			
			100					105					110					
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly			
	115						120					125						
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu			
	130					135					140							
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr			
145					150					155					160			
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn			
				165					170					175				
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe			
			180					185					190					
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn			
	195						200					205						

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 20

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)..(23)

<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>

<221> DOMAIN

<222> (24)..(240)

<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
 1 5 10 15

Pro Thr Pro Ser Pro Ser Cys Ala Pro Glu Leu Leu Gly Gly Pro Ser
 20 25 30

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 35 40 45

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 50 55 60

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 65 70 75 80

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 85 90 95

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 100 105 110


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Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
    115                      120                      125

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    130                      135                      140

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
    145                      150                      155                      160

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    165                      170                      175

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
    180                      185                      190

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
    195                      200                      205

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    210                      215                      220

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    225                      230                      235                      240

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<210> 21

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc_feature

<222> (1)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc_feature

<222> (814)..(1455)

<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21
aagcttgccg ccattgattt tcaagtgcag attttcagct tcttgctaatt cagtgtttca 60
gtcataaattg ccagaggaca aattgtttctc tcccagttctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc 300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgg 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
gtctattttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacagga ccacggtcac cgtctctgat ccaagaagg tggacaagat agaagatgaa 840
aggaatcttc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa 900
agatccttat ccttactgaa ctgtgaggag attaaaagcc agtttgaagg ctttgtgaag 960
gatataatgt taaacaaaga ggagacgaag aaagaaaaca gctttgaaat gcaaaaagg 1020
gatcagaatc ctcaaattgc ggcacatgct ataagtgagg ccagcagtaa aacaacatct 1080
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttgg aaccctggaa 1140
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc 1200
ttctgttcca atcggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag 1260
tccccggta gattcgagag aatcttactc agagctgcaa ataccacag ttccgcaaaa 1320
ccttgcgggc aacaatocat tcaattggga ggagtatttg aattgcaacc aggtgcttcg 1380
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt 1440
ggcttactca aactogagtg ataacttaga 1470

<210> 22

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc_feature

<222> (13)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc_feature

<222> (814)..(1275)

<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22

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aagcttgccg ccatggattt tcaagtgcag attttcagct tcttgctaata cagtgccttca      60
gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct      120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg      180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctgggt      240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc      300
agcagagtgg aggtgaaga tgctgocact tattactgcc agcagtggag tttaaccca      360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgg      420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg      480
aggcctgggg cctcagtga gatgtctgc aaggcttctg gctacacatt taccagttac      540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat      600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta      660
gacaaatcct ccagcacagc ctacatgcag ctacgcagcc tgacatctga agactctgcg      720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg      780

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ggcacagggg ccacgggtcac cgtctctgat ccagaaaaca gctttgaaat gcaaaaaggt      840
gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacaacatct      900
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggg aaccttgga      960
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc    1020
ttctgttcca atcgggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag    1080
tcccccggtg gattcgagag aatcttactc agagctgcaa atacccacag ttccgcaaaa    1140
ccttgcgggc aacaatccat tcaattggga ggagtatttg aattgcaacc aggtgcttcg    1200
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcaactggctt cacgtccttt    1260
ggcttactca aactcgagtg ataattctaga                                     1290

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<210> 23

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 23

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gtcaagcttg ccgcatgga ttttcaagtg cagatttttc agc      43
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<210> 24

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 24

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gtcgtcgagc tcccacctcc tccagatcca ccaccgccg agccaccgcc acctttcagc      60
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tccagcttgg tccc

74

<210> 25

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 25

gctgctgagc tctcaggctt atctacagca agtctgg

37

<210> 26

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 26

gttgtctgat cagagacggt gaccgtggtc cc

32

<210> 27

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 27

gttgatcgat ccagaaaaca gctttgaaat gcaa

34

<210> 28

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 28

gttgattcta gattatcact cgagtttgag taagccaaag gacg

44

<210> 29

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 29

gttgatcgat ccaagaaggt tggacaagat agaag

35

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 30

gtctatataa gcagagctct ggc

23

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 31

cgaggctgat cagcgagctc tagca

25

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 32

ccgcaatttg aggattctga tcacc

25

<210> 33

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(266)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> DOMAIN

<222> (268)..(481)

<223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	

Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			

Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
		50				55					60				

Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65					70					75					80

Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85					90					95	

Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		

Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			

Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135					140				

Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145					150					155					160

Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
				165					170					175	

Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
			180					185					190		

Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Leu Glu

<210> 34

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(266)

<223> MOUSE ANTI-HUMAN SCFV

<220>

<221>

DOMAIN

<222> (268)..(421)

<223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
 260 265 270
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 275 280 285
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 290 295 300
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
 305 310 315 320
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
 325 330 335
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
 340 345 350
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
 355 360 365
 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
 370 375 380
 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
 385 390 395 400
 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
 405 410 415

Gly Leu Leu Lys Leu Glu
420

<210> 35

<211> 63

<212> DNA

<213> Homo sapiens

<220>

<221> N region

<222> (1)..(63)

<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

<400> 35

ccagttccct caactccacc taccccatct cctcaactc cacctacccc atctccctca 60

tgc 63

<210> 36

<211> 21

<212> PRT

<213> Homo sapiens

<400> 36

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr
1 5 10 15

Pro Ser Pro Ser Cys
20

<210> 37

<211> 763

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(6)

<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>

<221> N_region

<222> (8)..(752)

<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

<400> 37
tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60
tcctcatgc tgccaccccc gactgtcact gcaccgaccg gccctcgagg acctgctctt 120
aggttcagaa gcgatcctca cgtgcacact gaccggcctg agagatgcct caggtgtcac 180
cttcacctgg acgccctcaa gtgggaagag cgctgttcaa ggaccacctg accgtgacct 240
ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccgagccat ggaaccatgg 300
gaagaccttc acttgactg ctgcctaccc cgagtccaag accccgctaa ccgccaccct 360
ctcaaaatcc ggaaacacat tccggcccga ggtccacctg ctgccgccgc cgtcggagga 420
gctggccctg aacgagctgg tgacgctgac gtgcctggca cgtggcttca gcccgaagga 480
tgtgtgtggt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540
ggcatcccg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg 600
cgtggcagcc gaggactgga agaaggggga caccttctcc tgcattgttg gccacgaggc 660
cctgccgtg gccttcacac agaagacct cgaccgcttg gcgggtaaac ccacccatgt 720
caatgtgtct gttgtcatgg cggaggtgga ctgataatct aga 763

<210> 38

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (3)..(250)

<223> TRUNCATED FORM, REMOVAL OF LAST THREE AMINO ACIDS THAT MEDIATE AT TACHMENT TO SECRETORY COMPONEN

<400> 38

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Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
1          5          10          15

Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg
          20          25          30

Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys
          35          40          45

Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr
          50          55          60

Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu
65          70          75          80

Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro
          85          90          95

Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser
          100          105          110

Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg
          115          120          125

Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn
          130          135          140

Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp
145          150          155          160

Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys
          165          170          175

Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr
          180          185          190

Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys
          195          200          205

Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala
210          215          220

Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val
225          230          235          240

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Asn Val Ser Val Val Met Ala Glu Val Asp
245 250